

CCT	COC	COC	CCT	GAG	COC	CCT	GTG	GAC	ACA	CTC	GTC	ATT	GTC	AGG	CAC	GAG	CGC	GTG	AAC
CGT	CGT	CGT	ACT	GAG	ACT	GAG	GAG	GAG	ACC	CTC	ACT	ACA	TTT	CGC	ACA	TTT	CGC	CGC	GAA
CAG	CAG	CAT	CTT	CTT	GCG	AGA	ACC	CTC	TCC	CTT	CTT	TGA	GAA	AGA	AAG	ATG	TGC	ATT	CGG
TAT	TCC	ACA	GAT	GAT	AAT	TTC	COC	TAT	CTC	ATC	TGC	TGC	TTC	AGG	ACC	ATG	AGG	ATG	AAA
TAC	ATC	CAG	CTT	GAG	CTT	GTG	GAG	TAC	TGC	ACC	TTT	CTG	CCT	GCA	GAT	A	R	V	K
CAG	ATC	Q	V	AGG	A	CTG	CCC	TCC	GCC	ATT	ATG	CAG	GCA	A	E	V	AGG	E	G
Q	I	Q	R	T	V	A	T	B	G	H	Q	A	V	E	L	L	D	L	C
ACC	TTC	AGT	AGA	AGA	GTG	TGC	GAG	CAA	TTT	GTG	ACT	CGG	GAA	TTT	GTG	AGG	CCC	CTC	CGG
T	L	E	K	G	V	W	H	L	Q	W	T	R	E	F	V	E	A	L	T
AQA	ACC	CGC	AGC	CTC	CTG	CCC	CGC	CTC	GAC	CCG	GAG	CTC	ACG	CTC	ACG	GAG	TTG	CCC	CTC
T	C	G	S	P	L	A	A	A	R	Y	H	E	P	E	L	T	D	L	P
CCA	TGT	TTG	GAG	AGC	GCT	CAT	GAT	AGA	TAT	CTC	CAA	TTC	ATC	CTC	CTC	GAG	CCC	ACT	T
CTG	GTG	GAG	GAG	E	CTT	CTA	CTT	AGA	GAG	TAT	L	Q	K	CTC	ATG	G	L	Q	P
L	V	D	K	L	L	V	R	D	V	L	D	F	C	M	E	E	E	L	L
ACA	ATT	GAA	GAG	AGA	AAC	CGG	ATT	GCT	CGT	CGA	GAA	AAC	AAT	GGA	AAT	GAA	TCA	GCT	GTG
T	I	E	D	R	R	I	A	A	A	A	E	H	S	G	H	E	S	G	V
AGA	GAG	CTA	CTA	AAA	AGG	ATT	GTG	CAG	AAA	GAA	ACA	TGG	TCT	CTC	CTT	CTG	AAT	GAT	TTT
R	H	L	L	K	R	I	V	Q	R	E	H	W	F	S	A	F	L	A	V
CTT	CGT	CAA	Q	ACA	GAG	AAT	AAA	CTT	GTG	CAA	GAG	TTA	ACA	CGC	TCT	GAT	TGC	TCA	GAA
AGC	ATC	H	L	F	E	K	E	H	E	F	G	ATG	CGT	CTT	CAA	GTG	GAG	CAA	CTT
S	E	A	E	I	E	H	L	C	Q	V	D	G	Q	V	G	E	E	Q	L
CTT	TCA	ACC	ACA	GTG	CAG	CCA	AAT	CTG	GAG	AGG	GAG	GTG	TGG	CGG	V	G	AGT	AAT	TCA
L	S	T	T	V	Q	P	H	E	L	E	K	E	V	W	G	H	E	H	S
TCA	GAA	TCA	TCT	TTT	GCA	GAT	TCT	TCT	GTG	ATT	TCA	GAA	TCA	ACA	ACA	AGT	TTG	GCA	GAA
S	E	S	S	F	A	D	S	S	S	V	S	E	S	H	D	T	S	L	A
GGA	AGT	GTG	AGC	TGC	TTA	GAT	GAA	AGT	CTT	GGA	CAT	AAC	AGC	AAC	ATG	GGC	AGT	GAT	TCA
CGC	ACC	ATG	AGA	AGT	GAT	TCA	GAT	AGA	GAG	ATG	GTG	GCA	ACA	AGA	ACA	TCC	CGC	AG	CA
G	T	H	Q	S	D	S	D	E	E	H	V	A	A	R	A	S	P	E	P
GAA	CTC	CAG	CTC	AGG	CGT	TAC	CAA	ATA	GAA	CTT	CGC	CAG	CCA	CGC	TTG	GAA	GGG	AGG	AAT
E	L	Q	C	L	R	P	Y	Q	H	E	V	A	Q	P	A	L	E	G	K
ATC	ATC	ATC	TGC	TGC	CTC	ACA	GGG	AGT	GGA	AAA	ACC	AGA	GTG	GCT	GTG	TAC	ATT	CCC	AAT
I	I	I	C	L	P	T	G	S	G	K	T	R	V	A	V	Y	A	I	A
GAT	CAG	TTA	GAG	CAG	AGG	AAA	ACA	GCA	TCT										

CATTGAACTC TTTTAAAGAA CACAATATAT TANGCATTAT CCATCTTATT
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CCAGTCTCAG TTCTGTCACT AATTTTCAGA **ATAAAATTAG** GCAAATCAGT
TC

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 E -MADKVLVFKRKLFIRSMGEGTINGLIDELLQTFVLNKKEEMKVKPEN-ATVMDKTRALI 58
 P1-453 -ASDDLSLIRKFNPMALFQQLTCVLPILONLLFANVINQEHDIHQY--TQPSLQARBLI 58
 P2-439 -ESNDLLSIRKFNRMALFQHLTCVLPILDSLLTAGIENEQEHDIHQY--TQPSLQARBLI 57
 H-1 -HHPHQBTDFKFNRVVLAQQLLSLEHLEHLEFDITTEMSBLIQAY--AGSFSQNVELL 57
 a5-125 -----LVDKLLVFDVDFCMEEELTIEDFNPIAAAEENNGNESGVPELL 44
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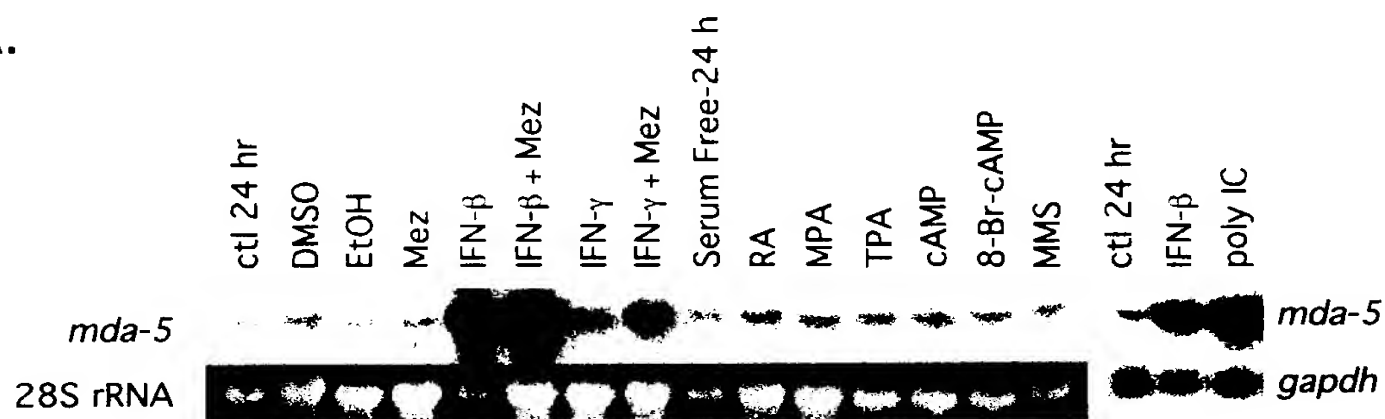
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 P1-453 DTILVKGNAANIFKNCLKEIDSTLY-----NLEVDKNNKYIP-----TEDVSGLSLEE 108
 P2-439 DTILVKGNIATVFPNSLQBAEAVLY-----EHLFVQQDIKYIP-----TEDVSDLPVEE 107
 H-1 NLLPKEGQAFDAFCALRETKQHLED--ALLTISGLQHVLPPLSCDYDLSLFPVCE 115
 a5-125 -RIVQK----- 50
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8RNAHelicase	-----MSGYSSDRDFGRDGFGEAFEGG-----	23
a-5	MELSTLEKGVVHLGWTFEPVEALRPTGSPLAAPYMNPETDLSPSPSFENAHDEYLQLNL	120
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F4A1	-----DGME-----EGVIESNWN--	28
8RNAHelicase	-----SPAGPLSGYFFGNP-----GEKLVTFFKNLD	49
a-5	MQFTLVDKLLVF DVIDKCMEEELTIEDFNIAAAEENNNGNESGVPELLEAPINQENWPSA	180
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F4A1	-----	
8RNAHelicase	EL-----EFTEYNFYQEHPDLARPTAQEVETYPFSKEITVRGH	87
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F4A1	---EIVDSFDMMNLS-----ESLLRGIIAYVG	51
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a-5	ENNSSESSPADSSVVVSSEDTSLAEGSVSCLDESIGHNSNMGSDSGTMGSDSDEENVAAPA	300
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a-5	SPEPELQLRPYQMEVAQPALEGKNIICLETGSGFTPVAVVIAYDHLDKFK--KASEPGK	358
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F4A1	ALVLAPTRELAAQQIQ-----	117
8RNAHelicase	CLVLAPTRELAAQQVQ-----	184
a-5	AVLVNKVLLVLEQLERKEFQPFELFWYPVIGLSGDTQLNISFPEVVKSCDIISTAQILE	418
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F4A1	-----EVV	120
8RNAHelicase	-----QVA	187
a-5	NSLLNLENGEDAGVQLSDPSLIIDECCHTNKEAVYNNIMPHYLMQKLNRRLLKENKPV	478
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8RNAHelicase	AHYCRACRLKSTCIYGGAPKGPQIRDLERG-VETCIATPGRLLIDPLECGKTNLRRTTYLV	246
a-5	IPLPQILGLTASPGVGGATKQAKAEHHILKLCANLDAPTIKTVENLDQLKNQIQEPCKK	538
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F4A1	LDEADEMLSRGFRKDQIIDIFQKLNSNTQVLLSATMPSDVLEVTKKFMRDPRIILVKKEE	240
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a-5	FAIADATREDPFKEKILLEIMTRIQTTCQMSPMSPDGTQPYEQWAIQMEKKAACKGNRKER	598
	: : : : : : : : : : : : : : : : :	
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8RNAHelicase	LSANHNILQ-----IVDVCHDEVKDEKLIR---	331
a-5	VCASHLRKYNEBALQINDIPMIDAYTHLETIFYNEEKDEKFAVEDDSDREGGDDEYCDGDE	658
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8RNAHelicase	-----LMEEIMSEKE-	341
a-5	DEDDLKKPLKLDDETDRFLMTLFFENNMKMKPLAENPEYENEKLTKLRLTIMEQYTRTES	718
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8RNAHelicase	NKTIYFVETKR-----RCDELTPMERDGGWPAMGIHG-----SQQEPDWVLNEF	387
a-5	ARGIIFTYKTPQSAYALSQWITENEKFAEVGVFAHHLIGAGHSSEFPYPMQTONEQYEVISKF	778
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a-5	TGKINLLIATTVAEEGLDIFEENIVIFYGLVTNETAMVQAAGRARADESTYVLAHSGS	838
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F4A1	VINMVTEEDKRTLRLDIETFYNTSIEMPLENVADLI-----	406
8RNAHelicase	LYTFPTFNNIKQVSDLISVCEANQAINPYLLQLVEDFGSGPSRGGPGMYDDRFDFYSAG	500
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A.



B.

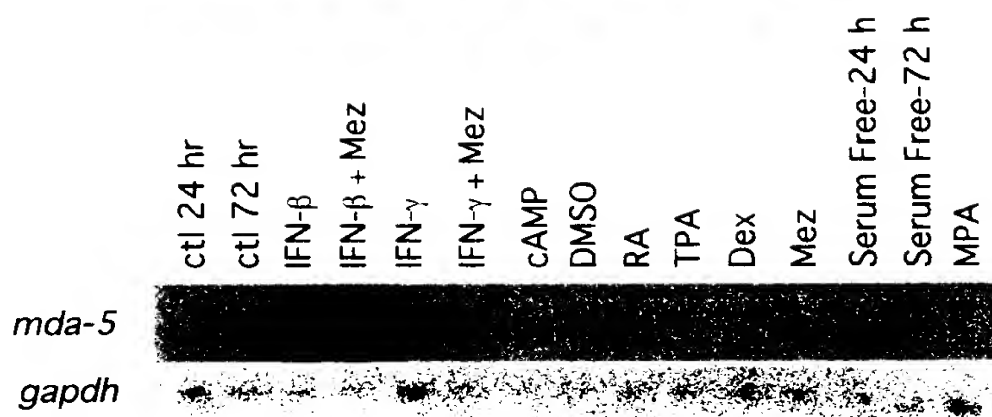
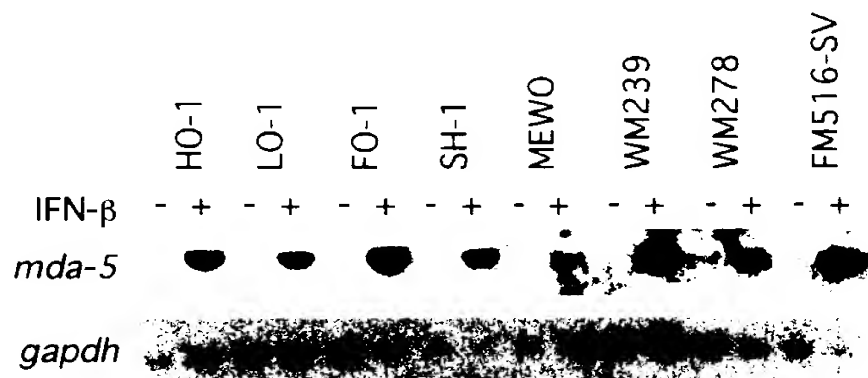


Figure 2

A.



B.

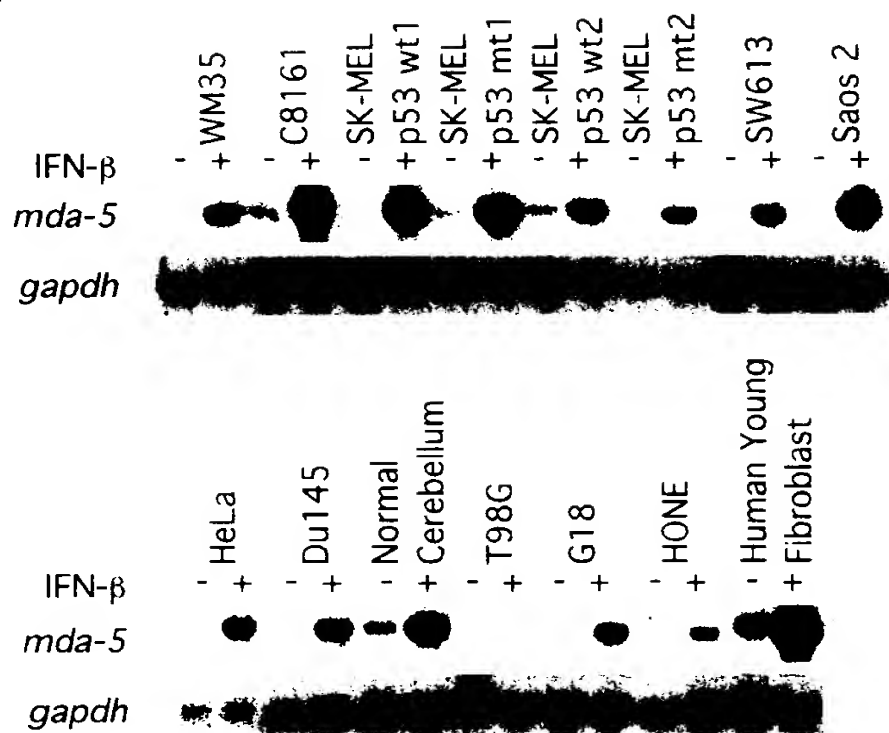
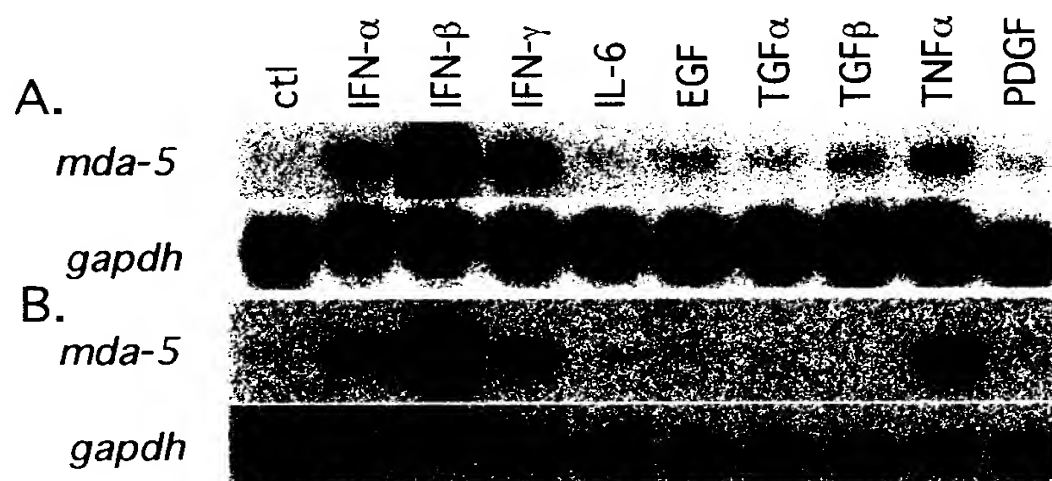


Figure 3



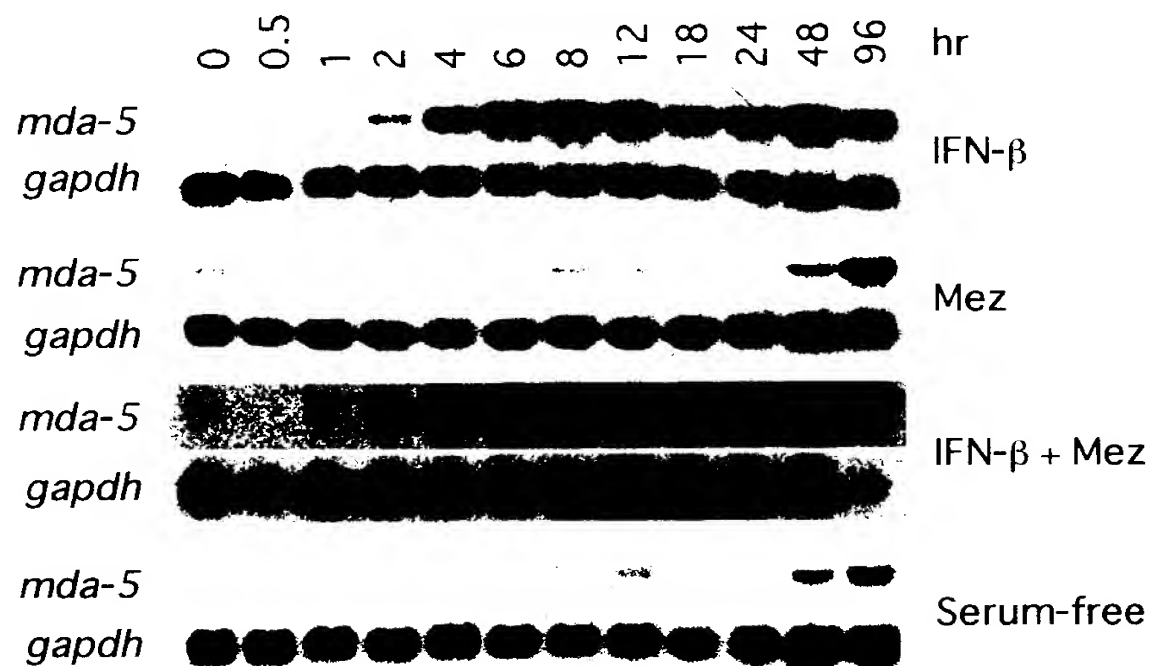


Figure 5

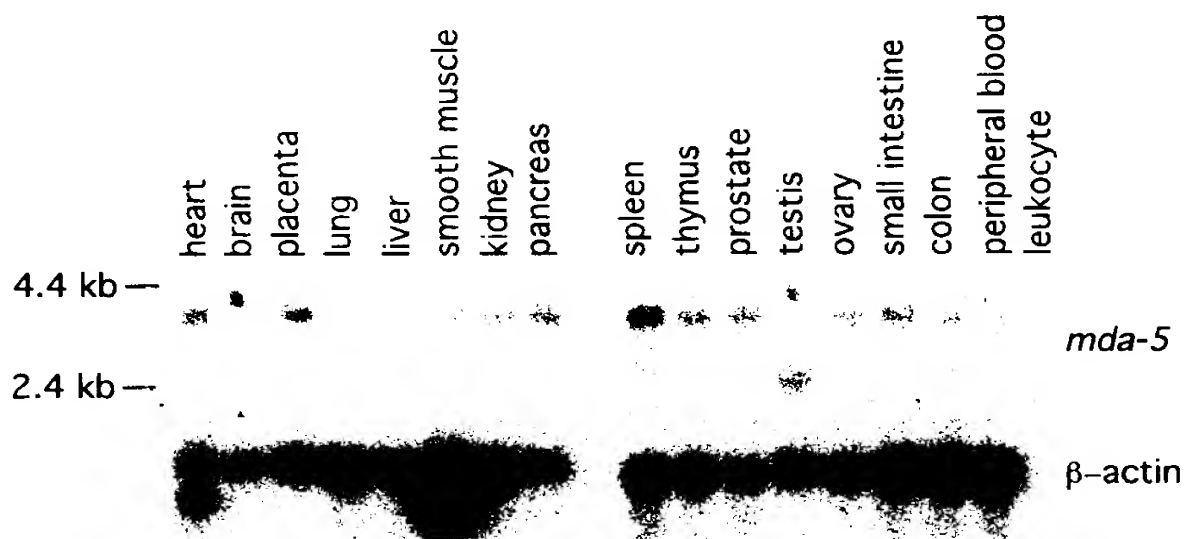
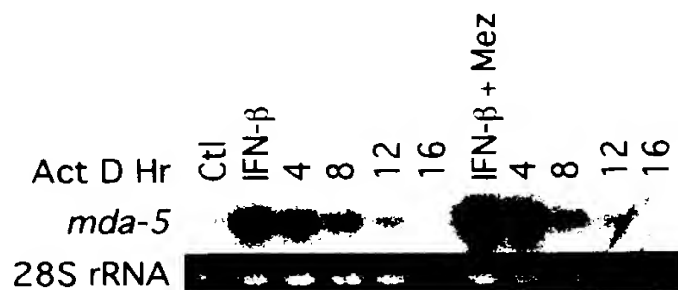
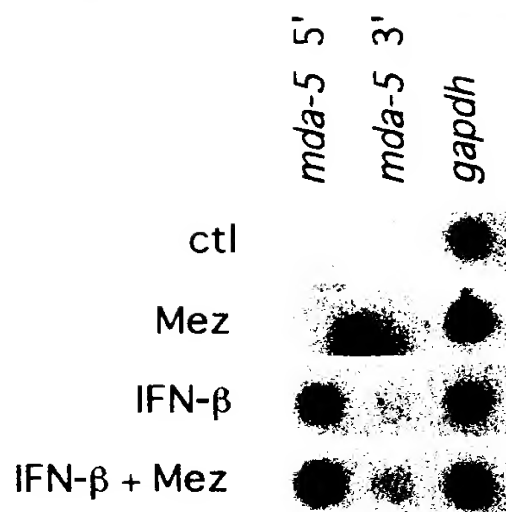


Figure 6

A.



B.



C.

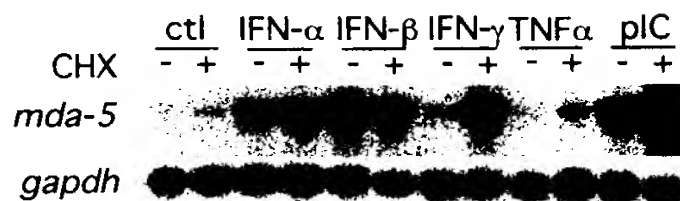
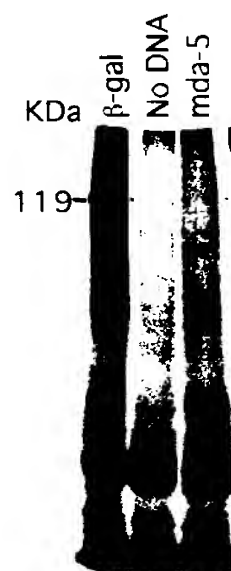
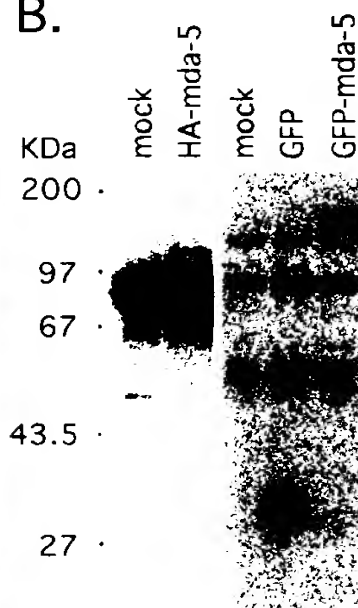


Figure 7

A.



B.



C.

